

ENTERED

1600

RAW SEQUENCE LISTING

DATE: 02/28/2002

PATENT APPLICATION: US/09/910,071

TIME: 09:28:42

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF3\02282002\I910071.raw

```
3 <110> APPLICANT: Tomikawa, Mayumi
             Aikawa, Seiichi
             Matsuzawa, Fumiko
      7 <120> TITLE OF INVENTION: Method and Apparatus for Extracting and Evaluating Mutually
Similar
             Portions in One-Dimensional Sequences in Molecules and/or Three-Dimensional
             Structures of Molecules
    11 <130> FILE REFERENCE: 522.1921D2
    13 <140> CURRENT APPLICATION NUMBER: 09/910,071
    14 <141> CURRENT FILING DATE: 2001-07-23
    16 <150> PRIOR APPLICATION NUMBER: US 08/014,867
    17 <151> PRIOR FILING DATE: 1993-02-08
                                                                      RECEIVED
    19 <160> NUMBER OF SEQ ID NOS: 20
    21 <170> SOFTWARE: PatentIn version 3.1
                                                                       MAR 1 3 2002
    23 <210> SEQ ID NO: 1
    24 <211> LENGTH: 37
                                                                    Technology Center 2100
    25 <212> TYPE: PRT
    26 <213> ORGANISM: human
    28 <400> SEQUENCE: 1
    30 Gly Asp Val Glu Lys Gly Lys Lys Ile Phe Ile Met Lys Cys Ser Gln
                                            10
    34 His Thr Val Glu Gly Gly Lys His Lys Thr Gly Pro Asn Leu His Gly
    35
                  20
                                        25
    38 Leu Phe Gly Arg Lys
              35
    42 <210> SEQ ID NO: 2
    43 <211> LENGTH: 39
    44 <212> TYPE: PRT
    45 <213> ORGANISM: bacterium
    47 <400> SEQUENCE: 2
    49 Glu Gly Asp Asp Ala Ala Ala Gly Glu Lys Val Ser Lys Lys Cys Leu
    53 Ala Cys His Thr Phe Asp Gln Gly Gly Ala Asn Lys Val Gly Pro Asn
                   20
                                        25
    57 Pro Asn Leu Phe Gly Val Phe
    61 <210> SEQ ID NO: 3
    62 <211> LENGTH: 51
    63 <212> TYPE: PRT
    64 <213> ORGANISM: rat
    66 <400> SEQUENCE: 3
    68 Met Ser Leu Ala Ile Leu Arg Val Ile Arg Leu Val Arg Val Phe Arg
    72 Ile Phe Lys Leu Ser Arg His Ser Lys Gly Leu Gln Ile Leu Gly Arg
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/910,071

DATE: 02/28/2002 TIME: 09:28:42

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF3\02282002\I910071.raw

25 76 Thr Leu Lys Ala Ser Met Arg Glu Leu Gly Leu Leu Ile Phe Phe Ile 35 40 80 Gly Val Val 50 81 84 <210> SEQ ID NO: 4 85 <211> LENGTH: 142 86 <212> TYPE: PRT 87 <213> ORGANISM: unknown 89 <220> FEATURE: 90 <223> OTHER INFORMATION: Figure 23A 92 <400> SEQUENCE: 4 94 Thr Glu Glu Gln Ile Ala Glu Phe Lys Glu Ala Phe Ser Leu Phe Asp 10 98 Lys Asp Gly Asp Gly Thr Ile Thr Thr Lys Glu Leu Gly Thr Val Met 25 102 Arg Ser Leu Gly Gln Asn Pro Thr Glu Ala Glu Leu Gln Asp Met Ile 106 Asn Glu Val Asp Ala Asp Gly Asn Gly Thr Ile Asp Phe Pro Glu Phe 110 Leu Thr Met Met Ala Arg Lys Met Lys Asp Thr Ser Glu Glu Glu Ile 114 Arg Glu Ala Phe Arg Val Phe Asp Lys Asp Gly Asn Gly Tyr Ile Ser 118 Ala Ala Glu Leu Arg His Val Met Thr Asn Leu Gly Glu Lys Leu Thr 100 105 122 Asp Glu Glu Val Asp Glu Met Ile Arg Glu Ala Asn Ile Asp Gly Asp 120 126 Gly Gln Val Asn Tyr Glu Glu Phe Val Gln Met Met Thr Ala 127 130 130 <210> SEQ ID NO: 5 131 <211> LENGTH: 159 132 <212> TYPE: PRT 133 <213> ORGANISM: unknown 135 <220> FEATURE: 136 <223> OTHER INFORMATION: Figure 23B 138 <400> SEQUENCE: 5 140 Ala Met Asp Gln Gln Ala Glu Ala Arg Ala Phe Leu Ser Glu Glu Met 144 Ile Ala Glu Phe Lys Ala Ala Phe Asp Met Phe Asp Ala Asp Gly Gly 148 Gly Asp Ile Ser Thr Lys Glu Leu Gly Thr Val Met Arg Met Leu Gly 152 Gln Asn Pro Thr Lys Glu Glu Leu Asp Ala Ile Ile Glu Glu Val Asp 55 156 Glu Asp Gly Ser Gly Thr Ile Asp Phe Glu Glu Phe Leu Val Met Val 70 160 Arg Gln Met Lys Glu Asp Ala Lys Gly Lys Ser Glu Glu Leu Ala 90

RAW SEQUENCE LISTING DATE: 02/28/2002 PATENT APPLICATION: US/09/910,071 TIME: 09:28:42

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF3\02282002\I910071.raw

164 Asp Cys Phe Arg Ile Phe Asp Lys Asn Ala Asp Gly Phe Ile Asp Ile 100 105 168 Glu Glu Leu Gly Glu Ile Leu Arg Ala Thr Gly Glu His Val Thr Glu 115 120 125 172 Glu Asp Ile Glu Asp Leu Met Lys Asp Ser Asp Lys Asn Asn Asp Gly 135 176 Arg Ile Asp Phe Asp Glu Phe Leu Lys Met Met Glu Gly Val Gln 177 145 150 180 <210> SEQ ID NO: 6 181 <211> LENGTH: 28 182 <212> TYPE: PRT 183 <213> ORGANISM: unknown 185 <220> FEATURE: 186 <223> OTHER INFORMATION: calmodulin probe site 81-108, Figure 25, target 188 <400> SEQUENCE: 6 190 Leu Ala Asp Cys Phe Arg Ile Phe Asp Lys Asn Ala Asp Gly Phe Ile 194 Asp Ile Glu Glu Leu Gly Glu Ile Leu Arg Ala Thr 195 20 198 <210> SEO ID NO: 7 199 <211> LENGTH: 28 200 <212> TYPE: PRT 201 <213> ORGANISM: unknown 203 <220> FEATURE: 204 <223> OTHER INFORMATION: calmodulin probe site 81-108, probe, Figure 25 206 <400> SEQUENCE: 7 208 Ile Arg Glu Ala Phe Arg Val Phe Asp Lys Asp Gly Asn Gly Tyr Ile 212 Ser Ala Ala Glu Leu Arg His Val Met Thr Asn Leu 213 20 216 <210> SEQ ID NO: 8 217 <211> LENGTH: 27 218 <212> TYPE: PRT 219 <213> ORGANISM: unknown 221 <220> FEATURE: 222 <223> OTHER INFORMATION: Calmodulin probe site 117-143, Figure 26, target 224 <400> SEQUENCE: 8 226 Ile Glu Asp Leu Met Lys Asp Ser Asp Lys Asn Asn Asp Gly Arg Ile 227 1 5 230 Asp Phe Asp Glu Phe Leu Lys Met Met Glu Gly 20 234 <210> SEQ ID NO: 9 235 <211> LENGTH: 27 236 <212> TYPE: PRT 237 <213> ORGANISM: unkown 239 <400> SEQUENCE: 9 241 Val Asp Glu Met Ile Arg Glu Ala Asn Ile Asp Gly Asp Gly Gln Val 245 Asn Tyr Glu Glu Phe Val Gln Met Met Thr Ala

DATE: 02/28/2002

TIME: 09:28:42

Input Set : A:\PTO.VSK.txt Output Set: N:\CRF3\02282002\I910071.raw 25 249 <210> SEQ ID NO: 10 250 <211> LENGTH: 8 251 <212> TYPE: PRT 252 <213> ORGANISM: unknown 254 <220> FEATURE: 255 <223> OTHER INFORMATION: Coordinates of C-alpha corresponding to the aminon acid residue N 256 os. 7 to 14 in elongation factor of protein which is a binding si 257 te for phosphoric acid of GTP 259 <400> SEQUENCE: 10 261 Gly His Val Asp His Gly Lys Thr 262 1 265 <210> SEQ ID NO: 11 266 <211> LENGTH: 8 267 <212> TYPE: PRT 268 <213> ORGANISM: unknown 270 <220> FEATURE: 271 <223> OTHER INFORMATION: adenylate kinase - target 273 <400> SEQUENCE: 11 275 Gly Ala Pro Gly Ser Gly Lys Gly 276 1 279 <210> SEO ID NO: 12 280 <211> LENGTH: 8 281 <212> TYPE: PRT 282 <213> ORGANISM: unknown 284 <220> FEATURE: 285 <223> OTHER INFORMATION: ras protein - target 287 <400> SEQUENCE: 12 289 Gly Ala Gly Gly Val Gly Lys Ser 290 1 293 <210> SEQ ID NO: 13 294 <211> LENGTH: 8 295 <212> TYPE: PRT 296 <213> ORGANISM: unknown 298 <220> FEATURE: 299 <223> OTHER INFORMATION: adenylate kinase (3ADK) 301 <400> SEQUENCE: 13 303 Gly Gly Pro Gly Ser Gly Lys Gly 304 1 307 <210> SEQ ID NO: 14 308 <211> LENGTH: 223 309 <212> TYPE: PRT 310 <213> ORGANISM: unknown 312 <220> FEATURE: 313 <223> OTHER INFORMATION: amino acid sequence of trypsin

317 Ile Val Gly Gly Tyr Thr Cys Cys Ala Asn Thr Val Pro Tyr Gln Val

321 Ser Leu Asn Ser Gly Tyr His Phe Cys Gly Gly Ser Leu Ile Asn Ser

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/910,071

315 <400> SEQUENCE: 14

318 1

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/910,071

DATE: 02/28/2002 TIME: 09:28:42

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF3\02282002\I910071.raw

322				2.0					25					30		
	Gln		37	20	Com	71	717	ui c		ጥ፣ረድ	Tare	Ser	Glv		Gln	Val
	Gin	Trp		vaı	ser	Ата	нта	40	Cys	TYL	шуз	501	45	110	0111	· u ·
326	Arg	Tou	35	Clu	λαη	λen	Tle		Va 1	Val	Glu	Glv		Glu	Gln	Phe
	Arg	ьец 50	GTĀ	GIU	АБР	ASII	55	W211	Val	Val	GIU	60		014	01	
330	Ile		λla	Car	Laze	Ser		Val	His	Pro	Ser		Asn	Ser	Asn	Thr
		Ser	Ата	361	ту	70	110	Vai	111.5	110	75	-1-		001		80
334	Leu	7 an	λan	N cn	Tlo		T.eu	Tle	T.vs	T.e.ii		Ser	Ala	Ala	Ser	
338	ьeu	ASII	ASII	АБР	85	Mec	пси	110	טעט	90	1,0	001			95	
3/1	Asn	Sar	λrσ	Val		Ser	Tle	Ser	Leu		Thr	Ser	Cvs	Ala	Ser	Ala
342	ASII	261	лту	100	ALU	001	110	001	105				-1-	110		
	Gly	Thr	Gln		Leu	Tle	Ser	Glv		Glv	Asn	Thr	Lys	Ser	Ser	Gly
346	GLY	T111	115	0,10	200		00-	120		1			125			-
	Thr	Ser		Pro	Asp	Val	Leu		Cvs	Leu	Lys	Ala	Pro	Ile	Leu	Ser
350	1111	130	-1-				135		- 1		-	140				
	Asp		Ser	Cvs	Lvs	Ser	Ala	Tyr	Pro	Gly	Gln	Ile	Thr	Ser	Asn	Met
	145	001	201	01-	-1-	150		•		•	155					160
	Phe	Cvs	Ala	Glv	Tvr	Leu	Glu	Gly	Gly	Lys	Asp	Ser	Cys	Gln	Gly	Asp
358		-1-		2	165			-	-	170	_				175	
	Ser	Gly	Gly	Pro	Val	Val	Cys	Ser	Gly	Lys	Leu	Gln	Gly	Ile	Val	Ser
362		-	-	180			_		185	-				190		
	Trp	Gly	Ser	Gly	Cys	Ala	Gln	Lys	Asn	Lys	Pro	Gly	Val	Tyr	Thr	Lys
366	•	-	195	_				200					205			
369	Val	Cys	Asn	Tyr	Val	Ser	Trp	Ile	Lys	Gln	Thr	Ile	Ala	Ser	Asn	
370		210					215					220				
373	373 <210> SEQ ID NO: 15															
		0/ 0,	₽Ŏ TI) NO	: 12											
374	<21															
375	<21:	1> L1 2> T	ENGTI YPE:	H: 2	39											
375 376	<21: <21: <21:	1> L1 2> T 3> O	ENGTI YPE: RGAN	H: 2: PRT ISM:	39	nown										
375 376 378	<21: <21: <21: <22:	1> L1 2> T1 3> 01 0> F1	ENGTI YPE: RGANI EATUI	H: 2: PRT ISM: RE:	39 un k i							. 6	71 -	-4		
375 376 378 379	<21: <21: <21: <22: <22:	1> L1 2> T' 3> 0: 0> F' 3> 0'	ENGTI YPE: RGANI EATUI THER	H: 2: PRT ISM: RE: INF	39 unki ORMA		: am	ino (acid	seq	uenc	e of	Ela	stas	e	
375 376 378 379 381	<21: <21: <21: <22: <22: <40:	1> L1 2> T' 3> 0: 0> F: 3> 0' 0> S:	ENGTI YPE: RGAN: EATU! THER EQUE!	H: 2: PRT ISM: RE: INF(unki unki ORMA' 15	TION										Tle
375 376 378 379 381 383	<21: <21: <22: <22: <22: <40: Val	1> L1 2> T' 3> 0: 0> F: 3> 0' 0> S:	ENGTI YPE: RGAN: EATU! THER EQUE!	H: 2: PRT ISM: RE: INF(unki unki ORMA' 15 Thr	TION				Asn					Gln	Ile
375 376 378 379 381 383 384	<21: <21: <21: <22: <22: <40: Val:	1> L1 2> T' 3> O' 0> F' 3> O' 0> S' Val	ENGTI YPE: RGANI EATUI THER EQUEI Gly	H: 2: PRT ISM: RE: INFO NCE: Gly	unk unk ORMA 15 Thr 5	TION Glu	Ala	Gln	Arg	Asn 10	Ser	Trp	Pro	Ser	Gln 15	
375 376 378 379 381 383 384 387	<21: <21: <22: <22: <40: Val: 1 Ser	1> L1 2> T' 3> O' 0> F' 3> O' 0> S' Val	ENGTI YPE: RGANI EATUI THER EQUEI Gly	H: 2: PRT ISM: RE: INF(NCE: Gly Tyr	unk unk ORMA 15 Thr 5	TION Glu	Ala	Gln	Arg Ser	Asn 10	Ser	Trp	Pro	Ser Cys	Gln 15	
375 376 378 379 381 383 384 387 388	<21: <21: <22: <22: <40: Val: 1 Ser	1> L1 2> T' 3> 0: 0> F: 3> 0' 0> S: Val	ENGTI YPE: RGAN: EATUI THER EQUEI Gly	H: 2: PRT ISM: RE: INF(NCE: Gly Tyr 20	unki ORMA 15 Thr 5 Arg	TION Glu Ser	Ala Gly	Gln Ser	Arg Ser 25	Asn 10 Trp	Ser Ala	Trp His	Pro Thr	Ser Cys 30	Gln 15 Gly	Gly
375 376 378 379 381 383 384 387 388	<21: <21: <21: <22: <22: <40: Val: 1 Ser	1> L1 2> T' 3> 0: 0> F: 3> 0' 0> S: Val	ENGTI YPE: RGAN: EATUI THER EQUE: Gly Gln	H: 2: PRT ISM: RE: INF(NCE: Gly Tyr 20	unki ORMA 15 Thr 5 Arg	TION Glu Ser	Ala Gly	Gln Ser Val	Arg Ser 25	Asn 10 Trp	Ser Ala	Trp His	Pro Thr	Ser Cys 30	Gln 15 Gly	Gly
375 376 378 379 381 383 384 387 388 391	<21: <21: <22: <22: <40: Val: 1 Ser	1> L1 2> T 3> O 0> F 3> O 0> S Val Leu Leu	ENGTI YPE: RGAN: EATUI THER EQUE: Gly Gln Ile 35	H: 2: PRT ISM: RE: INFO NCE: Gly Tyr 20 Arg	unki ORMA' 15 Thr 5 Arg	TION Glu Ser Asn	Ala Gly Trp	Gln Ser Val 40	Arg Ser 25 Met	Asn 10 Trp Thr	Ser Ala Ala	Trp His Ala	Pro Thr His 45	Ser Cys 30 Cys	Gln 15 Gly Val	Gly Asp
375 376 378 379 381 383 384 387 388 391 392 395	<21: <21: <22: <22: <40: Val: Ser Thr	1> L1 2> T' 3> O' 0> F' 3> O' 0> S' Val Leu Leu	ENGTI YPE: RGAN: EATUI THER EQUE: Gly Gln Ile 35	H: 2: PRT ISM: RE: INFO NCE: Gly Tyr 20 Arg	unki ORMA' 15 Thr 5 Arg	TION Glu Ser Asn	Ala Gly Trp Val	Gln Ser Val 40	Arg Ser 25 Met	Asn 10 Trp Thr	Ser Ala Ala	Trp His Ala His	Pro Thr His 45	Ser Cys 30 Cys	Gln 15 Gly Val	Gly Asp
375 376 378 379 381 383 384 387 388 391 392 395	<21: <21: <21: <22: <22: <40: Val: 1	1> Li 2> T' 3> O: 0> F: 3> O' 0> S: Val Leu Leu Glu 50	ENGTHYPE: RGANTHER EQUET Gly Gln Ile 35 Leu	H: 2: PRT ISM: RE: INFO NCE: Gly Tyr 20 Arg	unk DRMA 15 Thr 5 Arg Gln Phe	Glu Ser Asn Arg	Ala Gly Trp Val	Gln Ser Val 40 Val	Arg Ser 25 Met Val	Asn 10 Trp Thr	Ser Ala Ala Glu	Trp His Ala His	Pro Thr His 45 Asn	Ser Cys 30 Cys Leu	Gln 15 Gly Val Asn	Gly Asp Gln
375 376 378 379 381 383 384 391 392 395 396 399	<21: <21: <22: <22: <40 Val 1 Ser Thr Arg	1> Li 2> T' 3> O: 0> F: 3> O' 0> S: Val Leu Leu Glu 50	ENGTHYPE: RGANTHER EQUET Gly Gln Ile 35 Leu	H: 2: PRT ISM: RE: INFO NCE: Gly Tyr 20 Arg	unk DRMA 15 Thr 5 Arg Gln Phe	Glu Ser Asn Arg Gln	Ala Gly Trp Val	Gln Ser Val 40 Val	Arg Ser 25 Met Val	Asn 10 Trp Thr	Ser Ala Ala Glu	Trp His Ala His	Pro Thr His 45 Asn	Ser Cys 30 Cys Leu	Gln 15 Gly Val Asn	Gly Asp
375 376 378 379 381 383 384 387 388 391 392 395 396 400	<21: <21: <22: <22: <40 Val 1 Ser Thr Arg Asn 65	1> Li 2> T' 3> O' 0> F' 3> O' 0> S' Val Leu Leu Glu 50 Asn	ENGTH YPE: RGANT EATUR THER EQUE Gly Gln Ile 35 Leu	H: 2: PRT ISM: RE: INF(NCE: Gly Tyr 20 Arg Thr	unki ORMA' 15 Thr 5 Arg Gln Phe	Glu Ser Asn Arg Gln 70	Ala Gly Trp Val 55 Tyr	Gln Ser Val 40 Val	Arg Ser 25 Met Val Gly	Asn 10 Trp Thr Gly Val	Ser Ala Ala Glu Gln 75	Trp His Ala His 60 Lys	Pro Thr His 45 Asn	Ser Cys 30 Cys Leu Val	Gln 15 Gly Val Asn	Gly Asp Gln Pro 80
375 376 378 379 381 383 384 387 392 395 396 399 400 403	<21: <21: <22: <22: <40 Val 1 Ser Thr Arg Asn 65 Tyr	1> Li 2> T' 3> O' 0> F' 3> O' 0> S' Val Leu Leu Glu 50 Asn	ENGTH YPE: RGANT EATUR THER EQUE Gly Gln Ile 35 Leu	H: 2: PRT ISM: RE: INF(NCE: Gly Tyr 20 Arg Thr	unki DRMA' 15 Thr 5 Arg Gln Phe Glu Asp	Glu Ser Asn Arg Gln 70	Ala Gly Trp Val 55 Tyr	Gln Ser Val 40 Val	Arg Ser 25 Met Val Gly	Asn 10 Trp Thr Gly Val	Ser Ala Ala Glu Gln 75	Trp His Ala His 60 Lys	Pro Thr His 45 Asn	Ser Cys 30 Cys Leu Val	Gln 15 Gly Val Asn	Gly Asp Gln Pro 80
375 376 378 379 381 383 384 391 392 395 396 399 400 403 404	<21: <21: <22: <22: <40 Val 1 Ser Thr Arg Asn 65 Tyr	1> Li 2> T' 3> O' 0> F' 3> O' 0> S' Val Leu Leu Glu 50 Asn	ENGTHYPE: RGANTERATURE REQUES Gly Gln Ile 35 Leu Gly Asn	H: 2: PRT ISM: RE: INFO NCE: Gly Tyr 20 Arg Thr Thr	unki DRMA' 15 Thr 5 Arg Gln Phe Glu Asp 85	Glu Ser Asn Arg Gln 70 Asp	Ala Gly Trp Val 55 Tyr Val	Gln Ser Val 40 Val Val	Ser 25 Met Val Gly	Asn 10 Trp Thr Gly Val Gly 90	Ser Ala Ala Glu Gln 75 Tyr	Trp His Ala His 60 Lys Asp	Pro Thr His 45 Asn Ile	Ser Cys 30 Cys Leu Val	Gln 15 Gly Val Asn Val Leu 95	Gly Asp Gln Pro 80 Leu
375 376 378 379 381 383 384 387 392 395 396 400 403 404 407	<21: <21: <22: <22: <40: Val: 1	1> Li 2> T' 3> O' 0> F' 3> O' 0> S' Val Leu Leu Glu 50 Asn	ENGTHYPE: RGANTERATURE REQUES Gly Gln Ile 35 Leu Gly Asn	H: 2: PRT ISM: RE: INFO NCE: Gly Tyr 20 Arg Thr Thr	unki DRMA' 15 Thr 5 Arg Gln Phe Glu Asp 85	Glu Ser Asn Arg Gln 70 Asp	Ala Gly Trp Val 55 Tyr Val	Gln Ser Val 40 Val Val	Ser 25 Met Val Gly	Asn 10 Trp Thr Gly Val Gly 90 Ser	Ser Ala Ala Glu Gln 75 Tyr	Trp His Ala His 60 Lys Asp	Pro Thr His 45 Asn Ile	Ser Cys 30 Cys Leu Val	Gln 15 Gly Val Asn Val Leu 95	Gly Asp Gln Pro 80 Leu
375 376 378 379 381 383 384 387 395 395 396 400 403 404 407 408	<21: <21: <22: <22 < 40 Val 1 Ser Thr Arg Asn 65 Tyr Arg	1> Li 2> T' 3> O' 3> O' 0> F' 3> O' 0> S: Val Leu Glu 50 Asn Trp	ENGTHYPE: RGANTERATURE REQUETER GLY GLN Leu GLY Asn Ala	H: 2: PRT ISM: RE: INF(NCE: Gly Tyr 20 Arg Thr Thr Thr Gln 100	unki DRMA' 15 Thr 5 Arg Gln Phe Glu Asp 85 Ser	Glu Ser Asn Arg Gln 70 Asp	Ala Gly Trp Val 55 Tyr Val Thr	Gln Ser Val 40 Val Val Ala Leu	Ser 25 Met Val Gly Ala Asn 105	Asn 10 Trp Thr Gly Val Gly 90 Ser	Ser Ala Ala Glu Gln 75 Tyr	Trp His Ala His 60 Lys Asp Val	Pro Thr His 45 Asn Ile Ile	Ser Cys 30 Cys Leu Val Ala Leu 110	Gln 15 Gly Val Asn Val Leu 95 Gly	Gly Asp Gln Pro 80 Leu Val
375 376 378 379 381 383 384 387 395 395 396 400 403 404 407 408	<21: <21: <22: <22: <40 Val 1 Ser Thr Arg Asn 65 Tyr Arg Leu	1> Li 2> T' 3> O' 3> O' 0> F' 3> O' 0> S: Val Leu Glu 50 Asn Trp	ENGTHYPE: RGANTERATURE REQUETER GLY GLN Leu GLY Asn Ala	H: 2: PRT ISM: RE: INFO NCE: Gly Tyr 20 Arg Thr Thr Thr Gln 100 Ala	unki DRMA' 15 Thr 5 Arg Gln Phe Glu Asp 85 Ser	Glu Ser Asn Arg Gln 70 Asp	Ala Gly Trp Val 55 Tyr Val Thr	Gln Ser Val 40 Val Val Ala Leu	Ser 25 Met Val Gly Ala Asn 105	Asn 10 Trp Thr Gly Val Gly 90 Ser	Ser Ala Ala Glu Gln 75 Tyr	Trp His Ala His 60 Lys Asp Val	Pro Thr His 45 Asn Ile Ile	Ser Cys 30 Cys Leu Val Ala Leu 110 Tyr	Gln 15 Gly Val Asn Val Leu 95 Gly	Gly Asp Gln Pro 80 Leu
375 376 378 379 381 383 384 387 395 396 400 403 404 407 408 411 412	<21: <21: <22: <22: <40: Val: 1	1> Li 2> T' 3> O' 3> O' 3> O' 0> F' 3> O' 0> S: Val Leu Glu 50 Asn Trp Leu Pro	ENGTHYPE: RGANTERATURE REQUES Gly Gln Ile 35 Leu Gly Asn Ala Arg 115	H: 2: PRT ISM: RE: INFO NCE: Gly Tyr 20 Arg Thr Thr Thr Gln 100 Ala	unki DRMA' 15 Thr 5 Arg Gln Phe Glu Asp 85 Ser	Glu Ser Asn Arg Gln 70 Asp Val	Ala Gly Trp Val 55 Tyr Val Thr	Gln Ser Val 40 Val Val Ala Leu Leu 120	Ser 25 Met Val Gly Ala Asn 105 Ala	Asn 10 Trp Thr Gly Val Gly 90 Ser	Ser Ala Ala Glu Gln 75 Tyr Tyr Ser	Trp His Ala His 60 Lys Asp Val	Pro Thr His 45 Asn Ile Gln Cys 125	Ser Cys 30 Cys Leu Val Ala Leu 110 Tyr	Gln 15 Gly Val Asn Val Leu 95 Gly Ile	Gly Asp Gln Pro 80 Leu Val

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/910,071

DATE: 02/28/2002

TIME: 09:28:43

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF3\02282002\I910071.raw